



COPY OF PAPERS  
ORIGINALLY FILED

I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231 on	
April 15, 2002	
(Date of Deposit)	
Kenneth A. Gandy	
Name of Registered Representative	
<i>Kenneth A. Gandy</i>	
Signature	
April 15, 2002	
Date of Signature	

## IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re patent application of:	) Before the Examiner
	) Unknown
Loren J. Field, et al.	)
	) Group Art Unit
Filed December 18, 2001	) 1632
	)
Serial No.: 10/024,066	)
	)
CARDIOMYOCYTES WITH ENHANCED	)
PROLIFERATIVE POTENTIAL, AND	)
METHODS FOR PREPARING AND USING SAME	)

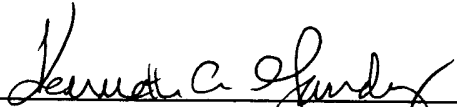
### **RESPONSE TO NOTICE TO FILE MISSING PARTS OF NONPROVISIONAL APPLICATION**

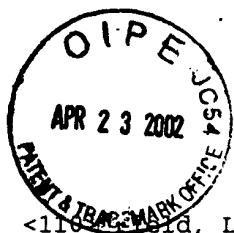
BOX MISSING PARTS  
Assistant Commissioner for Patents  
Washington, D.C. 20231

Sir:

In response to the Notice to File Missing Parts of Nonprovisional Application dated February 13, 2002, please find enclosed a copy of the Sequence Listing for which the original has been sent to "Box Sequence" and an executed Declaration/Power of Attorney form and check for the surcharge amount of \$130.00 as set forth in 37 CFR 1.16(l) for a large entity. Any additional necessary fees may be charged to or overpayment credited to Deposit Account No. 23-3030, but not to include payment of issue fees.

Respectfully Submitted,

By:   
Kenneth A. Gandy, Reg. No. 38386  
Woodard, Emhardt, Naughton,  
Moriarty & McNett  
Bank One Center/Tower  
111 Monument Circle, Suite 3700  
Indianapolis, Indiana 46204-5137  
(317) 634-3456



## SEQUENCE LISTING

&lt;110&gt; Cold, Loren J.

Pasumarthi, Kishore Babu S.

<120> CARDIOMYOCYTES WITH ENHANCED PROLIFERATIVE POTENTIAL,  
AND METHODS FOR PREPARING AND USING SAME

&lt;130&gt; 7037-450

&lt;140&gt; 10/024,066

&lt;141&gt; 2001-12-18

&lt;150&gt; 60/139,942

&lt;151&gt; 1999-06-18

&lt;150&gt; PCT/US00/16827

&lt;151&gt; 2000-06-19

&lt;160&gt; 8

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 876

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (4)..(870)

&lt;400&gt; 1

gct atg gag ctg ctg tgc tgc gag gtg gac ccg gtc cgc agg gcc gtg	48
Met Glu Leu Leu Cys Cys Glu Val Asp Pro Val Arg Arg Ala Val	
1 5 10 15	
ccg gac cgc aac ctg ctg gaa gac cgc gtt ctg cag aac ctg ttg acc	96
Pro Asp Arg Asn Leu Leu Glu Asp Arg Val Leu Gln Asn Leu Leu Thr	
20 25 30	
atc gag gag cgc tac ctc ccg cag tgt tcc tat ttc aag tgc gtg cag	144
Ile Glu Glu Arg Tyr Leu Pro Gln Cys Ser Tyr Phe Lys Cys Val Gln	
35 40 45	
aag gac atc caa ccg tac atg cgc agg atg gtg gcc acc tgg atg cta	192
Lys Asp Ile Gln Pro Tyr Met Arg Met Val Ala Thr Trp Met Leu	
50 55 60	

gag gtc tgt gag gaa caa aag tgt gaa gaa gag gtc ttt cct ctg gcc	240
Glu Val Cys Glu Glu Gln Lys Cys Glu Glu Glu Val Phe Pro Leu Ala	
65 70 75	
atg aat tac ctg gac cgt ttc ttg gct gga gtc ccg act cct aag acc	288
Met Asn Tyr Leu Asp Arg Phe Leu Ala Gly Val Pro Thr Pro Lys Thr	
80 85 90 95	
cat ctt cag ctc ctg ggt gca gtg tgc atg ttc cta gct tcc aag ctg	336
His Leu Gln Leu Leu Gly Ala Val Cys Met Phe Leu Ala Ser Lys Leu	
100 105 110	
aaa gag acc atc ccg ctg act gcg gaa aag ctg tgc att tac acc gac	384
Lys Glu Thr Ile Pro Leu Thr Ala Glu Lys Leu Cys Ile Tyr Thr Asp	
115 120 125	
aac tct gtg aag ccc cag gag ctg ctg gag tgg gaa ctg gta gtg ttg	432
Asn Ser Val Lys Pro Gln Glu Leu Leu Glu Trp Glu Leu Val Val Leu	
130 135 140	
ggt aag ctg aag tgg aac ctg gcc gca gtc acc cct cac gac ttc att	480
Gly Lys Leu Lys Trp Asn Leu Ala Ala Val Thr Pro His Asp Phe Ile	
145 150 155	
gag cac atc ctt cgc aag ctg ccc cag caa aag gag aag ctg tcc ctg	528
Glu His Ile Leu Arg Lys Leu Pro Gln Gln Lys Glu Lys Leu Ser Leu	
160 165 170 175	
atc cgc aag cat gcg cag acc ttc atc gct ctg tgc gct acc gac ttc	576
Ile Arg Lys His Ala Gln Thr Phe Ile Ala Leu Cys Ala Thr Asp Phe	
180 185 190	
aag ttt gcc atg tac ccg cca tcg atg att gca act gga agc gtg gga	624
Lys Phe Ala Met Tyr Pro Pro Ser Met Ile Ala Thr Gly Ser Val Gly	
195 200 205	
gca gcc atc tgt ggg ctt cag cag gat gat gaa gtg aac aca ctc acg	672
Ala Ala Ile Cys Gly Leu Gln Gln Asp Asp Glu Val Asn Thr Leu Thr	
210 215 220	
tgt gat gcc ctg act gag ctg ctg gcc aag atc acc cac act gat gtg	720
Cys Asp Ala Leu Thr Glu Leu Leu Ala Lys Ile Thr His Thr Asp Val	
225 230 235	
gat tgt ctc aaa gcc tgc cag gag caa atc gaa gct ctg ctg ctg aac	768
Asp Cys Leu Lys Ala Cys Gln Glu Gln Ile Glu Ala Leu Leu Leu Asn	
240 245 250 255	

agc ctg cag cag ttc cgt caa gag cag cat aac gcc gga tcc aag tct 816  
 Ser Leu Gln Gln Phe Arg Gln Glu Gln His Asn Ala Gly Ser Lys Ser  
                   260                  265                  270

gtg gaa gat ccg gac caa gcc acc acc cct aca gac gtg cgg gat gtt 864  
 Val Glu Asp Pro Asp Gln Ala Thr Thr Pro Thr Asp Val Arg Asp Val  
                   275                  280                  285

gac ctg tgagga 876  
 Asp Leu

<210> 2  
 <211> 289  
 <212> PRT  
 <213> Mus musculus

<400> 2  
 Met Glu Leu Leu Cys Cys Glu Val Asp Pro Val Arg Arg Ala Val Pro  
   1                  5                  10                  15

Asp Arg Asn Leu Leu Glu Asp Arg Val Leu Gln Asn Leu Leu Thr Ile  
                   20                  25                  30

Glu Glu Arg Tyr Leu Pro Gln Cys Ser Tyr Phe Lys Cys Val Gln Lys  
                   35                  40                  45

Asp Ile Gln Pro Tyr Met Arg Arg Met Val Ala Thr Trp Met Leu Glu  
                   50                  55                  60

Val Cys Glu Glu Gln Lys Cys Glu Glu Glu Val Phe Pro Leu Ala Met  
   65                  70                  75                  80

Asn Tyr Leu Asp Arg Phe Leu Ala Gly Val Pro Thr Pro Lys Thr His  
                   85                  90                  95

Leu Gln Leu Leu Gly Ala Val Cys Met Phe Leu Ala Ser Lys Leu Lys  
                   100                  105                  110

Glu Thr Ile Pro Leu Thr Ala Glu Lys Leu Cys Ile Tyr Thr Asp Asn  
                   115                  120                  125

Ser Val Lys Pro Gln Glu Leu Leu Glu Trp Glu Leu Val Val Leu Gly  
                   130                  135                  140

Lys Leu Lys Trp Asn Leu Ala Ala Val Thr Pro His Asp Phe Ile Glu  
   145                  150                  155                  160

His Ile Leu Arg Lys Leu Pro Gln Gln Lys Glu Lys Leu Ser Leu Ile  
165 170 175

Arg Lys His Ala Gln Thr Phe Ile Ala Leu Cys Ala Thr Asp Phe Lys  
180 185 190

Phe Ala Met Tyr Pro Pro Ser Met Ile Ala Thr Gly Ser Val Gly Ala  
195 200 205

Ala Ile Cys Gly Leu Gln Gln Asp Asp Glu Val Asn Thr Leu Thr Cys  
210 215 220

Asp Ala Leu Thr Glu Leu Leu Ala Lys Ile Thr His Thr Asp Val Asp  
225 230 235 240

Cys Leu Lys Ala Cys Gln Glu Gln Ile Glu Ala Leu Leu Leu Asn Ser  
245 250 255

Leu Gln Gln Phe Arg Gln Glu Gln His Asn Ala Gly Ser Lys Ser Val  
260 265 270

Glu Asp Pro Asp Gln Ala Thr Thr Pro Thr Asp Val Arg Asp Val Asp  
275 280 285

Leu

<210> 3

<211> 873

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (4)..(870)

<400> 3

gct atg gag ctg ctg tgc cac gag gtg gac ccg gtc cgc agg gcc gtg 48  
Met Glu Leu Leu Cys His Glu Val Asp Pro Val Arg Arg Ala Val  
1 5 10 15

cgg gac cgc aac ctg ctc cga gac gac cgc gtc ctg cag aac ctg ctc 96  
Arg Asp Arg Asn Leu Leu Arg Asp Asp Arg Val Leu Gln Asn Leu Leu  
20 25 30

acc atc gag gag cgc tac ctt ccg cag tgc tcc tac ttc aag tgc gtg	144
Thr Ile Glu Glu Arg Tyr Leu Pro Gln Cys Ser Tyr Phe Lys Cys Val	
35 40 45	
cag aag gac atc caa ccc tac atg cgc aga atg gtg gcc acc tgg atg	192
Gln Lys Asp Ile Gln Pro Tyr Met Arg Arg Met Val Ala Thr Trp Met	
50 55 60	
ctg gag gtc tgt gag gaa cag aag tgc gaa gaa gag gtc ttc cct ctg	240
Leu Glu Val Cys Glu Glu Gln Lys Cys Glu Glu Glu Val Phe Pro Leu	
65 70 75	
gcc atg aat tac ctg gac cgt ttc ttg gct ggg gtc ccg act ccg aag	288
Ala Met Asn Tyr Leu Asp Arg Phe Leu Ala Gly Val Pro Thr Pro Lys	
80 85 90 95	
tcc cat ctg caa ctc ctg ggt gct gtc tgc atg ttc ctg gcc tcc aaa	336
Ser His Leu Gln Leu Leu Gly Ala Val Cys Met Phe Leu Ala Ser Lys	
100 105 110	
ctc aaa gag acc agc ccg ctg acc gcg gag aag ctg tgc att tac acc	384
Leu Lys Glu Thr Ser Pro Leu Thr Ala Glu Lys Leu Cys Ile Tyr Thr	
115 120 125	
gac aac tcc atc aag cct cag gag ctg ctg gag tgg gaa ctg gtg gtg	432
Asp Asn Ser Ile Lys Pro Gln Glu Leu Leu Glu Trp Glu Leu Val Val	
130 135 140	
ctg ggg aag ttg aag tgg aac ctg gca gct gtc act cct cat gac ttc	480
Leu Gly Lys Leu Lys Trp Asn Leu Ala Ala Val Thr Pro His Asp Phe	
145 150 155	
att gag cac atc ttg cgc aag ctg ccc cag cag cgg gag aag ctg tct	528
Ile Glu His Ile Leu Arg Lys Leu Pro Gln Gln Arg Glu Lys Leu Ser	
160 165 170 175	
ctg atc cgc aag cat gct cag acc ttc att gct ctg tgt gcc acc gac	576
Leu Ile Arg Lys His Ala Gln Thr Phe Ile Ala Leu Cys Ala Thr Asp	
180 185 190	
ttt aag ttt gcc atg tac cca ccg tcg atg atc gca act gga agt gtg	624
Phe Lys Phe Ala Met Tyr Pro Pro Ser Met Ile Ala Thr Gly Ser Val	
195 200 205	
gga gca gcc atc tgt ggg ctc cag cag gat gag gaa gtg agc tcg ctc	672
Gly Ala Ala Ile Cys Gly Leu Gln Gln Asp Glu Glu Val Ser Ser Leu	
210 215 220	

act tgt gat gcc ctg act gag ctg ctg gct aag atc acc aac aca gac 720  
 Thr Cys Asp Ala Leu Thr Glu Leu Leu Ala Lys Ile Thr Asn Thr Asp  
 225 230 235

gtg gat tgt ctc aaa gct tgc cag gag cag att gag gcg gtg ctc ctc 768  
 Val Asp Cys Leu Lys Ala Cys Gln Glu Gln Ile Glu Ala Val Leu Leu  
 240 245 250 255

aat agc ctg cag cag tac cgt cag gac caa cgt gac gga tcc aag tcg 816  
 Asn Ser Leu Gln Gln Tyr Arg Gln Asp Gln Arg Asp Gly Ser Lys Ser  
 260 265 270

gag gat gaa ctg gac caa gcc agc acc cct aca gac gtg cgg gat atc 864  
 Glu Asp Glu Leu Asp Gln Ala Ser Thr Pro Thr Asp Val Arg Asp Ile  
 275 280 285

gac ctg tga 873  
 Asp Leu

<210> 4

<211> 289

<212> PRT

<213> Homo sapiens

<400> 4

Met Glu Leu Leu Cys His Glu Val Asp Pro Val Arg Arg Ala Val Arg  
 1 5 10 15

Asp Arg Asn Leu Leu Arg Asp Asp Arg Val Leu Gln Asn Leu Leu Thr  
 20 25 30

Ile Glu Glu Arg Tyr Leu Pro Gln Cys Ser Tyr Phe Lys Cys Val Gln  
 35 40 45

Lys Asp Ile Gln Pro Tyr Met Arg Arg Met Val Ala Thr Trp Met Leu  
 50 55 60

Glu Val Cys Glu Glu Gln Lys Cys Glu Glu Glu Val Phe Pro Leu Ala  
 65 70 75 80

Met Asn Tyr Leu Asp Arg Phe Leu Ala Gly Val Pro Thr Pro Lys Ser  
 85 90 95

His Leu Gln Leu Leu Gly Ala Val Cys Met Phe Leu Ala Ser Lys Leu  
 100 105 110

Lys Glu Thr Ser Pro Leu Thr Ala Glu Lys Leu Cys Ile Tyr Thr Asp



115	120	125
Asn Ser Ile Lys Pro Gln Glu Leu Leu Glu Trp Glu Leu Val Val Leu		
130	135	140
Gly Lys Leu Lys Trp Asn Leu Ala Ala Val Thr Pro His Asp Phe Ile		
145	150	155 160
Glu His Ile Leu Arg Lys Leu Pro Gln Gln Arg Glu Lys Leu Ser Leu		
165	170	175
Ile Arg Lys His Ala Gln Thr Phe Ile Ala Leu Cys Ala Thr Asp Phe		
180	185	190
Lys Phe Ala Met Tyr Pro Pro Ser Met Ile Ala Thr Gly Ser Val Gly		
195	200	205
Ala Ala Ile Cys Gly Leu Gln Gln Asp Glu Glu Val Ser Ser Leu Thr		
210	215	220
Cys Asp Ala Leu Thr Glu Leu Leu Ala Lys Ile Thr Asn Thr Asp Val		
225	230	235 240
Asp Cys Leu Lys Ala Cys Gln Glu Gln Ile Glu Ala Val Leu Leu Asn		
245	250	255
Ser Leu Gln Gln Tyr Arg Gln Asp Gln Arg Asp Gly Ser Lys Ser Glu		
260	265	270
Asp Glu Leu Asp Gln Ala Ser Thr Pro Thr Asp Val Arg Asp Ile Asp		
275	280	285

Leu

<210> 5  
 <211> 5443  
 <212> DNA  
 <213> Mus musculus

<400> 5  
 ggatcctgca aggtcacaca agggctctcca cccaccaggt gccctagtct caatttcagt 60  
 ttccatgcct tggtctcaca atgctggcct ccccagagct aatttgagct ttgtttttat 120  
 ttcaaaaggg cctgaatgag gagtagatct tgtgctaccc agctctaagg gtgcccgtga 180  
 agccctcaga cctggagcct ttgcaacagc ccttttaggtg gaagcagaat aaagcaattt 240  
 tccttaaagc caaatcctg cctctagact cttcttctct gacctcggtc cctgggctct 300

aggggtgggga ggtggggcctt ggaagaagaa ggtggggaag tggcaaaagc cgatccctag 360  
 ggccctgtga agttcggagc cttccctgtg cagcactggc tcatagatcc tcctccagcc 420  
 aaacatagca agaagtgata cctcctttgt gacttcccca ggcccagtac ctgtcagggtt 480  
 gaaacaggat ttagagaagc ctctgaactc acctgaactc tgaagctcat ccaccaagca 540  
 agcacctagg tgccactgct agttagtatc ctacgctgat aatatgcaga gctggggccac 600  
 agaagtcctg ggggtgtagga actgaccagt gacttttcag tcggcaaagg tatgaccccc 660  
 tcagcagatg tagtaatgtc cccttagatc ccatcccagg caggtctcta agaggacatg 720  
 ggatgagaga tgtagtcatg tggcattcca aacacagcta tccacagtgt cccttgcccc 780  
 ttccacttag ccaggaggac agtaacctta gcctatcttt ctccctcccc atcctcccag 840  
 gacacacccc ctggtctgca gtattcattt cttccttcac gtccccctctg tgacttccat 900  
 ttgcaaggct tttgacctct gcagctgctg gaagatagag tttggcccta ggtgtggcaa 960  
 gccatctcaa gagaaagcag acaacagggg gaccagattt tggaaggatc aggaactaaa 1020  
 tctactggcg gcctgggggt agaaaaaaga gtgagttagt ccgctccagc taagccaagc 1080  
 tagtccccga gatactctgc cacagctggg ctgctcgggg tagctttagg aatgtgggtc 1140  
 tgaaagacaa tgggattgga agacatctct ttgagtctcc cctcaacccc acctacagac 1200  
 aactcgtgt gtggccagac tcctgttcaa cagccctctg tgttctgacc actgagctag 1260  
 gcaaccagag catggggccct gtgctgagga tgaagagttg gttaccaata gcaaaaacag 1320  
 caggggaggg agaacagaga acgaaataag gaaggaagaa ggaaaggcca gtcaatcaga 1380  
 tgcaatcaga agagatggga agccaacaca cagcttgagc agaggaaaca gaaaaggag 1440  
 agattctggg cataaggagg ccacagaaag aagagcccag gcccccaag tctcctcttt 1500  
 ataccctcat cccgtctccc aattaagccc actcttcttc ctagatcaga cctgagctgc 1560  
 agcgaagaga cccgtaggga ggatcacact ggatgaagga gatgtgtgga gaagtccagg 1620  
 gcaacctaag agccagagcc taaaagagca agagataaag gtgcttcaa ggtggccagg 1680  
 ctgtgcacac agagggtcga ggactggttg tagagcctca agataaggat gatgctcaga 1740  
 atgggcgggg ggggggattc tggggggggg agagagaagg tgagaaggag cctggaacag 1800  
 agaactctgga agcgtctgga acgataccat aaagggaaga acccaggcta ccttttagatg 1860  
 taaatcatga aagacaggga gaagggaagc tggagagagt agaaggacct cggggcaaga 1920  
 catggaagca aggacaagcc aggttgagcg ctccgtgaaa tcagcctgct gaaggcagag 1980  
 ccctggtatg agcaccagaa cagcagaggc tagggttaat gtcgagacag ggaacagaag 2040  
 gtagacacag gaacagacag agacggggga gccaggtaac aaaggaatgg tccttctcac 2100  
 ctgtggccag agcgtccatc tgtgtccaca tactctagaa tgttcatcag actgcagggc 2160  
 tggcttggga ggcagctgga aagagtatgt gagagccagg ggagacaagg gggcctagga 2220  
 aaggaagaag agggcaaacc aggccacaca agagggcaga gcccagaact gagttaactc 2280  
 cttccttggt gcatcttcca taggaggcag tgggaactct gtgaccacca tccccatga 2340  
 gccccacta cccataccaa gtttggcctg agtggcattc taggttccct gaggacagag 2400  
 cctggccttt gtctcttgga cctgacccaa gctgacccaa tgttctcagt accttatcat 2460  
 gccctcaaga gcttgagaac caggcagtga catattaggc catgggctaa ccctggagct 2520  
 tgcacacagg agcctcaagt gacctccagg gacacagctg cagacagggt gcctttatcc 2580  
 ccaaagagca accatttggc atagggtggt gcaaagggga atgcaagggt gaatcagggtc 2640  
 ccttcaagaa tactgcatgc aagacctaag acccctggag agaggggtat gctcctgccc 2700  
 ccaccacca taaggggagt gaactatcct agggggctgg cgaccttggg gagacaccac 2760  
 attactgaga gtgctgagcc cagaaaaact gaccgcctg tgcctgccc acctccacac 2820  
 tctagagcta tattgagagg tgacagtaga taggggtggga gctggtagca gggagagtgt 2880  
 tcctgggtgt gaggggttag gggaaagcca gagcagggga gtctggcttt gtctcctgaa 2940  
 cacaatgtct acttagttat aacaggcatg acctgctaaa gaccaacat ctacgacctc 3000  
 tgaaaagaca gcagccctgg aggacagggg ttgtctctga gccttgggtg cttgatgggtg 3060  
 ccacaaagga gggcatgagt gtgagtataa ggccccagga gcgttagaga agggcacttg 3120  
 ggaaggggtc agtctgcaga gccctatcc atggaatctg gagcctgggg ccaactgggtg 3180

taaatctctg ggcctgccag gcattcaaag cagcacctgc atcctctggc agcctgggga 3240  
 ggcggaaggg agcaaccccc cacttatacc ctttctccct cagccccagg attaacacct 3300  
 ctggccttcc cccttccac ctcccatcag gaggggaggg ttgcagaggg agggtaaaaa 3360  
 cctacatgtc caaacatcat ggtgcacgat atatggatca gtatgtgtag aggcaagaaa 3420  
 ggaaatctgc aggcttaact gggttaatgt gtaaagtctg tgtgcatgtg tgtgtgtctg 3480  
 actgaaaacg ggcattggctg tgcagctgtt cagtctctgt cgtgagggtta ccagactgca 3540  
 ggtttgtgtg taaattgccc aaggcaaagt gggatgaatcc cttccatggt ttaaagagat 3600  
 tggatgatgg cctgcatctc aaggaccatg gaaaatagaa tggacactct atatgtgtct 3660  
 ctaagctaag gtagcaaggt ctttggagga cacctgtcta gagatgtggg caacagagac 3720  
 tacagacagt atctgtacag agtaaggaga gagaggaggg ggtgtagaat tctcttacta 3780  
 tcaaagggaa actgagtcgt gcacctgcaa agtggatgct ctccctagac atcatgactt 3840  
 tgtctctggg gagccagcac tgtggaactt cagggtctgag agagtaggag gctccccctca 3900  
 gcctgaagct atgcagatag ccagggttga aagggggaag ggagagcctg ggatgggagc 3960  
 ttgtgtgttg gaggcagggg acagatatta agcctggaag agaagggtgac ccttaccag 4020  
 ttgttcaact cacccttcag attaaaaata actgaggtaa gggcctgggt aggggagggtg 4080  
 gtgtgagacg ctctgtctc tctctatct gcccatcggc ctttgggga ggaggaaatgt 4140  
 gcccaaggac taaaaaaagg ccatggagcc agaggggga gggcaacaga ctttcatgg 4200  
 gcaaaccttg gggccttctg gtctctctgt cacctccaga gccaaggat caaaggagga 4260  
 ggagccagga caggaggga gtgggaggga ggggtccagc agaggactcc aaatttaggc 4320  
 agcaggcata tgggatggga tataaagggg ctggagcact gagagctgtc agagatttct 4380  
 ccaaccag taagaggag tttcgggtgg gggctcttca cccacaccag acctctccc 4440  
 acctagaagg aaactgcctt tctggaagt ggggttcagg ccggtcagag atctgacagg 4500  
 gtggccttcc accagcctgg gaagtctca gtggcaggag gttccacaa gaaacactgg 4560  
 atgccccctc ccttacgtg tcttctccat ctctctctg gggatgctc tccccgtctt 4620  
 ggtttatctt ggctcttctg ctctcagcaag atttgccctg tctgttccac tccatcttct 4680  
 tctactgtct ccgtgccttg ccttgcttct ttgctgtctc tctcttcca cccatttctc 4740  
 acttcacctt ttctccccct ctcatcttga ttcattcttct ctctcttct tcttctctc 4800  
 ctctcttct tcttctctc ctttctctct tcttctctc ctctctctc tcttctctc 4860  
 ctctctctc gtgtcagagt gctgagaatc acacctggg ttcccacct tatgtaaaaca 4920  
 atcttccagt gagccacagc ttcagtgtg ctgggtgtc tcttacctc ctcacccct 4980  
 ggcttgtctt gttccatctt ggtcaggatc tctagattgg tctcccagc tctgtactc 5040  
 ctcttctctg ctgttctct ctctgtccag ctgcgccact gtggtgcctc gttccagctg 5100  
 tgggtccacat tcttcaggat tctctgaaa gttaaccagg tgagaatgtt tcccctgtag 5160  
 acagcagatc acgattctcc cggaagtcag gcttccagc ctctcttct ctgcccagct 5220  
 gcccggcact cttagcaaac ctcaggcacc cttacccac atagacctct gacagagaag 5280  
 caggcacttt acatggagtc ctgggtggg agccataggc tacgggtgaa aagaggcagg 5340  
 gaagtgggtg tgtaggaaa tcaggacttc acatagaagc ctagcccaca ccagaaatga 5400  
 cagacagatc cctctatct ccccataag agtttgagtc gac 5443

<210> 6

<211> 134

<212> DNA

<213> Simian virus 40

<400> 6

gtggatgggc agcctatgat tggaatgtcc tctcaagtag aggagggttag ggtttatgag 60  
 gacacagagg agcttctctg ggatccagac atgataagat acattgatga gtttggacaa 120

accacaacta gaat

134

<210> 7

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 7

gctatggagc tgctgtgctg cgaggtggac

30

<210> 8

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 8

tcctcacagg tcaacatccc gcacgtctgt

30